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Length=1255
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Length=1255			
Score = 2602 bits (6744), Expect = 0.0, Method: Compositional matrix adjust. Identities = $1255/1255$ (100%), Positives = $1255/1255$ (100%), Gaps = $0/1255$ (0%)			
Query Sbjct	1	MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQDLFL MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTOHTSSMRGVYYPDEIFRSDTLYLTQDLFL MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTOHTSSMRGVYYPDEIFRSDTLYLTQDLFL	60 60
Query	61	PPYSNVTGFHTINHTFGNPVIPPKDGIYFAATEKSNVVRGWVFGSTMNKSQSVIIINN: PFYSNVTGPHTINHTFGNPVIPPKDGIYFAATEKSNVVRGWVFGSTMNKSQSVIIINN: PFYSNVTGPHTINHTFGNPVIPPKDGIYFAATEKSNVVRGWVFGSTMNKSQSVIIINN:	120
Sbjct	61		120
Query	121	TNVVIRACNFELCDNPFFAVSKPMGTQTHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFK TNVVIRACNFELCDNPFFAVSKPMGTQTHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFK	180
Sbjct	121	TNVVIRACNFELCONPFFAVSKPMGTÕTHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFK	180
Query	181	HLREFVFKNKDGFLYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSP HLREFVFKNKDGFLYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSP	240
Sbjct	181	HLREFVFKNKDGFLYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSP	240
Query	241	AQDIWGTSAAAYFVGYLKPTTPHLKYDENGTITDAVDCSQNPLAELKCSVKSFEIDKGI AQDIWGTSAAAYFVGYLKPTTPHLKYDENGTITDAVDCSQNPLAELKCSVKSFEIDKGI AQDIWGTSAAAYFVGYLKPTTPHLKYDENGTITDAVDCSQNPLAELKCSVKSFEIDKGI	300
Sbjct	241		300
Query	301	QTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFPSVYAMERKKISNCVADYSVLYNST GTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFPSVYAMERKKISNCVADYSVLYNST QTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFPSVYAMERKKISNCVADYSVLYNST	360
Sbjct	301		360
Query	361	FSTEKCYGVSATKINDLCFSNVYADSFVVKGDDVRQIAPGGTCV1ADVNYKLPDDPMGCV FSTEKCYGVSATKINDLCFSNVYADSFVVKGDDVRQIAPGGTCV1ADVNYKLPDDPMGCV FSTEKCYGVSATKINDLCFSNVYADSFVVKGDDVRQIAPGGTCV1ADVNYKLPDDPMGCV LAWNTKNIDATSTGNYNYKRYLRHGKLRPPERDISNVPSPDGRGCTPPALNCVWELNI LAWNTKNIDATSTGNYNYKRYLRHGKLRPPERDISNVPSPDGRGCTPPALNCVWELNI LAWNTKNIDATSTGNYNYKRYLRHGKLRPPERDISNVPSPDGRGCTPPALNCVWELNI	420
Sbjct	361 421		420 480
Query	421		480
Sbjct	481	LAWMINNIDAISIGNINIKIKIKANGKLREFENDISMYEFSFUGEVLIPFALMU. INFLMU YGFYTTTGIGYQPYRVVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTP YGFYTTTGIGYQPYRVVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTP YGFYTTTGIGYQPYRVVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTP	540
Query Sbjct	481		540
Query	541	SSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQD	600
Sbjct	541	SSKRFÖPFÖÖFGRDVSDFTDSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYÖD SSKRFÖPFÖÖFGRDVSDFTDSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYÖD	600
Query	601	${\tt VNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASY}$	660
Sbjct	601	VNCTDVSTAIHADÕLTPAWRIYSTGNNVFÕTÕAGCLIGAEHVDTSYECDIPIGAGIO VNCTDVSTAIHADQLTPAWRIYSTGNNVFÕTÕAGCLIGAEHVDTSYECDIPIGAGIO	660
Query	661	HTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDC HTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDC	720
Sbjct	661	HTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDC	720
Query	721	NMYICGDSTECANLLLQYGSFCTOLNRALGGIAAEQDRNTEEVFAQVKOMYKTPILK NMYICGDSTECANLLLQYGSFCTOLNRALGGIAAEQDRNTEEVFAQVKOMYKTPILK NMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKOMYKTPILKY	780
Sbjct	721		780
Query	781	GFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNG GFNFSOILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAOKFNG	840
Sbjct	781	GFNFSÖILPDPLKPTKRSFIEDLLFNKVTLADAGFMKÖYGECLGDINARDLICAÖKFNGL	840
Query	841	TVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYE TVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYE	900
Sbjct	841	TVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYE	900
Query	901	NQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLI NQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLI	960
Sbjct	901	NQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN	960
Query	961	DILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSK DILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSK DILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSK	1020
Sbjct	961		1020
Query	1021	RVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVFVFN RVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVFVFN DVDFCCGVUHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVFVFN DVDFCCGVUHLMSFPQAAPHGVAFHUTTAPAICHEGKAYFPREGVFVFN	1080
Sbjct	1021	RVDFCGKGYHLMSFPÖAAPHGVVFLHVTYVPSÖERNFTTAPAICHEGKAYFPREGVFVF GTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFK	1140
Query Sbjct	1081	GTSWFITQRNFFSPQIITIDNTFVSGNCDVVIGIINNTVIDPLQFELDSFREELDKFFRN GTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQFELDSFREELDKYFKN	1140
Ouerv	1141	HTSPDVDLGDISGINASVVNIOKEIDRLNEVAKNLNESLIDLOELGKYEOYIKWPWYVWL	1200
*1		HTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWL	

Sbjct 1141 HTSPDVDLGDISGINASVVNIOKEIDRLNEVAKNLNESLIDLOELGKYEOYIKWPWYVWL 1200 GFIAGLIAIVMVTILLCCMTSCCSCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT GFIAGLIAIVMVTILLCCMTSCCSCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT GFIAGLIAIVMVTILLCCMTSCCSCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT Query 1201 1255 1255